TCCAGCTCCTGGGCGAATCCCACATCTGTTTCAACTCTCCGCGAGGGCGAGCAGGAGCGAGAGTGTGTGAATCTGCG AGTGAAGAGGGACGAGGGAAAAGAAACAAAGCCACAGACGCAACTTGAGACTCCCGCATCCCAAAAAAAGGACCAGATC

CGCGTCCGGGCAGATTCACGTCGTTTCCAGCCAAGTGGACCTGATCGATGGCCCTCCTGAATTTATCACGATATTTGAT

16	36	56	76	96	116	136
48	108	168		288	348	408
H H C	Q CAG	V GTG	T ACG	CIC	CCC	Y TAC
V GTG	T T T	D GAT	G GGG	I ATC	S TCG	9 9 9
T	R	Q		S	S	T
ACT (AGG	CAG	GGC	TCC	TCC	ACT
A	0	D	Q	S	C	S
GCA	0	GAC	CAG	TCC	HGC	AGC
S	K	D	E	CGC	N	N
TCC (AAA	GAC	GAG		AAC	AAT
L	L	T	M	S	E	CHC
CTG	CTG	ACG	ATG	TCA	GAG	
L	R	L	I	CCC	N	Y
TTG (CGC	CTG	ATC		AAT	TAC
C TGC	H CAC	V GTG	R CGC	C H G C	N AAC	V GTG
L	H	L	R	C	T	A
CTG	CAC	CTG	CGG	TGC	ACC	GCC
V	S	I	T	M	Y	F
GTG (TCG	ATC	ACC	ATG	TAC	
L CTC (L	I ATC	K AAG	P	T ACC	T ACC
S AGC (H H C	N AAC	N AAC	T ACA	N AAC	R CGC
P	A	P	M	T	H	S
CCG	GCC	CCC	ATG	ACC	CAC	AGC
CCC	S	R CGC	V GTG	V GTG	N AAC	E GAG
	S	I	Q		H	H
9	AGC	ATC	CAG	TTC	CAC	CAC
M	G	N	M	A	V	Q
ATG	GGA	AAC	ATG	GCC	GTC	CAG
	GGT	R AGG	S	N AAC	Y TAC	A GCA
1AAG	Γ	R GGC	GGT	I ATC	K AAG	Q CAG
AGCAAAAAAAGAAG	L	D GAC	CIG	FTC	GGC	W TGG
AGC?	S TCC	R AGG	E	H CAC	T ACC	S TCC

Fig. 1A

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156 468	176 528	196 588	216 648	236	256 768	276 828	296 888	316 948
9 9	R CGG	I ATC	V GTC	S TCA	P	ACC	T ACG	A GCC
P	C TGT	L	P CCA	Y TAT	N AAC	H H H C	E GAG	T ACC
P CCA	L	D GAC	R AGG	Q CAA	CCC	E GAA	M ATG	m Y TAC
V GTG	T ACG	T ACA	H CAC	P CCA	A GCG	M ATG	S TCC	V GTA
Y TAC	Y TAC	CIC	P	A GCC	YTAC	H CAC	D GAC	I ATC
S TCC	N AAC	m Y	Y TAC	S TCA	N AAC	I ATC	D GAC	YTAC
G GGC	Y TAT	D GAT	M ATG	D GAT	YTAC	P	V GTG	T ACG
N AAC	E E E E	K AAG	K AAG	E GAG	S AGC	K AAG	S TCG	N AAC
YTAC	R CGC	S TCC	K AAG	P CCT	P CCG	M ATG	M ATG	D GAC
E	S TCC	Y TAC	S TCC	G GGC	T ACG	P	L	$_{ m L}$
N AAT	N AAC	D GAC	T ACG	H CAC	I ATC	G GGG	T ACC	E GAG
L	K AAA	S	R	P	H CAC	T ACG	Q CAG	G GGC
Y TAT	L	G GGC	H H H C	A GCC	Q CAG	Y TAC	$rac{ ext{L}}{ ext{TTG}}$	T ACG
K AAG	CIC	H CAC	H H C	A GCA	S TCT	R CGC	G G G	E GAG
GGG	G GGA	K AAG	S AGC	H CAT	A GCA	M ATG	K AAG	V GTT
F TTC	V GTC	E GAG	V GTG	S AGC	N AAC	I ATC	R CGG	L
F TTC	W TGG	K AAA	S AGC	I ATC	P CCA	W TGG	Q CAG	M ATG
A GCT	E GAG	V GTG	D GAC	V GTC	H H H C	H CAC	CIC	N AAC
T ACA	K AAG	GGG	N AAT	M ATG	CIC	K AAA	M ATG	Y TAC
R CGG	W	N AAC	ACC	CIC	CGC	D GAC	N AAC	I ATT

Fig. 1B

				3/30				
336 1008	356 1068	376 1128	396 1188	416 1248	436 1308	456 1368	476 1428	496 1488
EGAG	N AAT	D GAC	V GTG	R AGA	L CTG	E GAG	K AAG	YTAC
$egin{array}{c} Y \ TAT \end{array}$	L CIG	L CHG	P CCG	EGAG	T T T	C TGT	H CAT	K AAG
P CCA	C TGT	GGC	R CGG	V GTG	N AAC	A GCG	L	CCC
M ATG	GGC	A GCA	E GAG	L TTG	E GAG	T ACG	K AAG	V GTG
S TCC	A GCC	I ATT	T ACG	F TTC	E GAG	Q CAG	L	CIC
K AAA	E GAA	D GAC	D GAC	S	Q CAG	Y TAC	K AAG	N AAC
999	V GTG	L CTG	L CTG	D GAC	A GCC	E GAG	G GGG	S TCC
K AAA	N AAC	I ATC	L	R CGG	D GAC	A GCT	T ACG	L
V GTG	P CCC	TACC	K AAG	W TGG	V GTG	R CGT	A GCC	A GCC
CIG	G GGC	PCCC	CIC	V GTC	K AAG	Q CAG	D GAC	R AGA
U U U	R AGG	A GCC	I ATC	R AGG	D GAC	C TGT	E GAG	S AGC
H H H H	V GTG	L	S TCC	M ATG	N AAT	L	V GTG	GGC
Q CAG	Y TAC	D GAC	K AAA	K AAG	D GAC	D GAC	C TGT	G.G.C
GGC	F TTC	I ATT	G GG	K AAG	R AGA	K AAG	Q CAG	L CTG
I ATC	P	N AAC	D GAC	K AAA	K AAG	V GTG	W	R CGG
H CAC	V GTC	CIC	M ATG	T.T.G	H CAC	R CGT	K AAG	M ATG
Y TAC	R AGG	V GTC	D GAT	H CAC	L CTA	Q CAG	Q CAG	P
G GGT	I ATC	I ATC	A GCG	F	CIG	Y TAC	GGA	GGC
H CAC	D GAC	H CAC	PCCT	R CGG	K AAG	K AAG	$_{ m L}$	K AAG
D GAC	H H H	PCCC	I ATA	N AAT	9 9	P	Q CAG	C IBC

Fig. 1(

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1548	1608	1668	1728	1788	1848	1908	1968	2028
A	S	A	D	P	D	E	R	K
GCC	TCC	GCC	GAC		GAC	GAA	CGG	AAG
L	R CGC	D GAT	D GAT	N AAC	L CTG	I ATT	K AAG	CIC
S	S	G	Q	A	D	E	K	R
AGC	AGT		CAA	GCC	GAC	GAG	AAA	CGC
CIC	R	L	D	A	C	H	K	9
	CGC	CTG	GAC	GCC	TGT	CAC	AAG	9
K	V	9	E	S	Q	D	L	K
AAG	GTC	9	GAG	TCA	CAG	GAC	CTG	AAA
Y	Y	V	PCCT	Y	V	I	H	H
TAC	TAT	GTA		TAC	GTC	ATC	CAC	CAC
D	S	H	A	D	T	H	G	Q
GAC	AGC	CAC	GCC	GAC	ACA	CAC	GGT	CAG
999	A GCC	Y TAC	G GGG	PCCC	D GAC	L CIG	R CGA	TACC
S	K	V	P	L	N	K	V	H
AGC	AAG	GTG	CCA		AAC	AAG	GTC	CAC
D	Y	R	W	295	E	H	E	Y
GAC	TAC	AGG		GGC	GAG	CAC	GAA	TAC
C	K	9	H	G	L	D	R	S
TGT	AAG	GGC	CAC	GGA	CTA	GAC	AGG	AGC
T ACC	K AAG	D GAC	R CGG	TACT	I ATC	K AAA	L	I ATC
C H G G	K AAG	V GTG	K AAG		Y TAC	W TGG	N AAC	K AAA
A	F	E	T	S	C	A	K	H
GCC	TTC	GAG	ACC	AGT	TGC	GCC	AAG	CAC
E	CIC	I ATC	CIC	F	R CGG	Q CAG	I ATT	$_{ m TGT}$
S	K	A	N	D	H	L	K	D
AGC	AAA	GCC	AAC	GAC	CAT		AAA	GAC
U U U U	K AAA	V GTG	R CGA	G GGG	T ACA	S TCC	N AAC	$_{\rm TGT}^{\rm C}$
Q CAG	R CGG	S TCA	CCC	G	V GTG	K AAG	Q CAG	E GAA
G	R	R	Q	D	K	Y	Γ	E
GGG	CGC	CGC	CAG	GAT	AAA	TAC		GAA
Y TAC	GGA	IATC	A GCC	K AAG	I ATT	L	TACC	P CCA

Fig. 11

	Ц
>	GIG
X	AAG
Ω	GAC
×	AAG
臼	GAG
Q	CAA
Н	CTG
ტ	GGC
凶	AAG
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Ы	CCI
Н	CAT
Н	CIG
ഗ	AGT
ß	CC

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				3 / 30				
696 2088	716 2148	736 2208	756 2268	776 2328	796 2388	816 2448	836 2508	856 2568
\overline{W}	N AAC	Q CAG	T ACG	T ACT	N AAC	C E U	GGA	P CCT
V GTG	Q CAG	W TGG	N AAC	A GCA	V GTG	S AGC	D GAT	R AGA
K AAG	L	H CAC	N AAT	F	A GCA	R AGG	K AAA	K AAG
D GAC	R CGC	Q CAG	N AAC	E GAA	N AAT	L CIG	L	M ATG
K AAG	K AAG	N AAC	A GCC	$_{\rm TGT}^{\rm C}$	M ATG	E GAG	G GGA	E GAA
E GAG	CIC	D GAC	S AGC	F	L CIG	M ATG	Γ	P CCA
Q CAA	L CIG	H CAC	T ACC	L	Q CAG	CIC	D GAC	W
L CTG	K AAG	T ACC	C H&C	F TTC	YTAC	Q CAG	M ATG	K AAG
G GGC	R CGC	F F T C	A GCC	N AAT	PCCC	V GTA	N AAC	R CGA
K AAG	CIC	C AGC	$^{ m C}$	H CAC	D GAC	H CAC	R CGA	R CGT
R AGG	K AAA	T ACG	F TTC	T ACT	T ACA	L CTA	TACT	Q CAG
F TTC	K AAG	L	PCCT	E GAG	N AAC	Q CAG	R CGG	F TTT
P	K AAG	S GGC	GGG	N AAT	L	N AAC	P CCC	Q CAG
H CAT	R CGC	P CCA	L	I ATC	D GAT	L	N AAC	R AGG
L	K AAG	M ATG	T ACA	T ACC	F TTT	V GTC	C	m Y TAC
S AGT	Q CAG	S AGC	W TGG	R AGG	m Y TAC	D GAT	Q CAG	Q CAA
S	E GAG	C TGC	F TTC	M ATG	E GAG	R AGG	K AAG	E GAG
G GGC	R CGG	T ACG	PCCT	C TGC	L CTA	D GAC	Y TAC	m Y TAT
R AGA	m L	D GAC	A GCG	W TGG	F TTC	L	G	s AGC
H CAC	L	N AAC	T ACG	Y TAC	GGC	T ACA	K AAG	G GGA

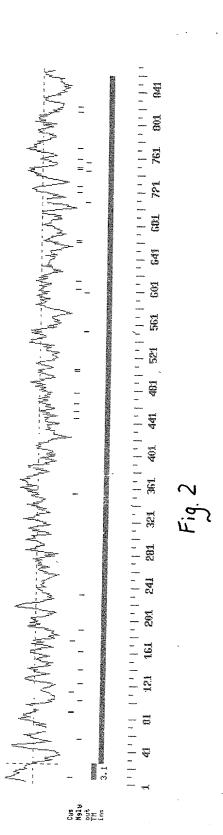
870 2613

GAAACAACAGAGGIGGACCICCAAAAACAIAGAGGCAICACCIGACIGCACAGGCAAIGAAAAACCAIGIGGGIGAIII TAACCAGCAGGAGCAGAGATAACTTCAGGAAGTCCATTTTTGCCCCTGCTTTTGCTTTTGGATTATACCTCACCAGCTGC CGAGAGAGATTTCCTTGGAAATTTCTCCCAAGGGCGAAAGTCATTGGAATTTTTAAATCATAGGGGAAAAGCAGTCCTG TTCTAAATCCTCTTATTCTTTTGGTTTGTCACAAAGAAGGAACTAAGAAGCAGGACAGGACAGGCAACGTGGAGAGGCTGAA AACAGTGCAGAGACGTTTGACAATGAGTCAGTAGCACAAAAGAGATGACATTTACCTAGCACTATAAACCCTGGTTGCC TCTGAAGAAACTGCCTT

Fig. 1F

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22437	GAGCGAGAGTGTCGAGTGTGTGCGTCTGTGTGTCCCGGCGAGGGTGCGCGCTCGGC
22437	
1247	GCCGGGAGCCGGCCAGCCGGAGGCATCGGGAGGTCGAGAGCCGCCGGGACCCCC 120 110 120
22437	
1247	AGCTCTGCGTTCACTCCCGTCCGGAGCTGGACTTCGGGGCCCGGGGCCCGGGGCCGTGCG
22437	
1247	CCGGGGACAGGCCGGGTCGCGGGCCGCGTCCCCCAGGCCGGAGATCTGCGAGT

Fig. 3A

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22437				 	 	
1247	GAAGAGGGACAAGGAAAAAAAGCCACAGAGGCAACTTGAGACTCCCGCATCCCA 250 250 260 270 280 290	saaagaaacaa 260	AGCCACAGACO 270	scaacttgag <i>i</i> 280	ACTCCCGCATC 290	300
22437	 	 	ATGGGC(10 ccccgagcc	10 20 ATGGGCCCCCGAGCCTCGTGCTTG	30 TTG
1247	AAAGAAGCACCAGA'	::::::::::::::::::::::::::::::::::::::	:::::: AGAAGATGGGCC 330	::::::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	360 360
!	40 50 60 70 80 90 90	50	09) O L	80 TGTCGCACCAC	90
22437	CTGTCCGCAACTGT					• • •
1247	CTGTCCGCAACTGTGTTCTCCCTGCTGGGTGGAAGCTCGGCCTTCCTGTCGCACCACCGC 370 380 390 400 410	GTTCTCCCTGCI 380	rgggtggaagg 390	TCGGCCTTCC 400	TGTCGCACCAC 410	3CGC 420
22437	150 130 140 150 130 140 150 CIGAAAGGCCAGGTTTCAGAGGGACCGCAGGAACATCCGCCCCAACATCATCTGGTGCTG	110 TCAGAGGGACCG	120 3CAGGAACATC	130 .cgccccaaca	140 TCATCCTGGTC	150 3CTG
1247	CTGAAAGGCAGGTTTCAGAGGACCGCAGGAACATCCGCCCCAACATCATCTGGTGCTG A50 480	GCAGGTTTCAGAGGACCGCAGGAACATCCGCCCCAACATCATCC	::::::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	:::: GCTG 480
	430	4.4.0	007	0) •	

Fig. 31

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10 kg 15 kg 16 kg 16 kg
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	160	170	180	190	200	210
22437	ACGGACGACCAGGA	CGACCAGGATGTGGAGCTGGGTTCCATGCAGGTGATGAACAAGACCCGGCGCATC	STICCAIGCA	SGTGATGAACA	AGACCCGGCG	CATC
12.47						
†	490	500	510	520	530	540
		230	240	250	7.09.Z	270
75477	ATGGAGCAGGGCGG	GCAGGGCGGGACGCACTTCATCAACGCCTTCGTGACACACAC	ICAACGCCII)))
1247	ATGGAGCAGGGCGG	GCAGGGCGGGACGCACTTCATCAACGCCTTCGTGACCACACCCCATGTGCTGCCCC	TCAACGCCTT	CGTGACCACAC	CCATGTGCTG	2000
	550	560	570	580	590	009
	280	290	300	310	320	330
22437	TCACGCTCCTCCAT	CICCICCAICCICACGGCAAGIACGICCACAACCACAACACTACACCAACAAI	AGTACGTCCA	CAACCACAACA	CCTACACCAA	CAAT
170			· · · · · · · · · · · · · · · · · · ·		・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・	·· E
/ 471	ICACGCICCICCAI 610	620	630	640	650	099
	0.20	с С	7	370	380	000
22437	GAGAACTGCTCCTC	CIGCICCICGCCTCCIGGCAGGCACAGCACGAGAGCCGCACCITIGCCGTGTAC	ggg Aggcacagca	SGAGAGCCGCA	CCTTTGCCGT	GTAC
	••		••		•••	••
1247	GAGAACTGCTCCTC	CTGCTCCTCGCCCTCCTGGCAGGCACAGCACGAGGCCGCACCTTTGCCGTGTAC	AGGCACAGCA	CGAGAGCCGCA	CCTTTGCCGT	GTAC
	670	089	069	700	710	720

Fig. 30

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Title: "22437, A Novel Human Sulfatase and Uses Therefor"
Inventors: Maria A. Glucksmann et al.
U.S. Patent Appl. No.: Not Yet Assigned
Express Mail # EL665882062US Attorney Docket No. 10147-61U1 Cust # 570

2737	400	450 440 450 430 440 450 430 440 450 450	420 TTTCTTCGGG	430 AAGTATCTTA <i>l</i>	440 ATGAATACAAC	450 GGC
1247	CICAAIAGCACIGGCCTCCCCCCCCCCCCCCCCCCCCCCC	1866601860186018601861861861861861861861861861861861861861	.:::::::: TTTCTTCGGG/ 750	.:::::: \AGTATCTTA/ 760	::::::::::::::::::::::::::::::::::::::	::: 666 780
22437	460 TCCTACGTGCCACC(:::::::::::::::::::::::::::::::::	460 470 480 490 500 510 CGTGCCACCCGGCTGGAGGGGTCGGACTCCTTAAAAACTCCCGCTTTTAT ::::::::::::::::::::::::::::::::	480 GTGGGTCGGA(::::::::: GTGGGTCGGA(810	490 CTCCTTAAAAA :::::::::	500 ACTCCCGCTTT' :::::::: ACTCCCGCTTT 830	510 TAT ::: TAT 840
22437	520 530 540 550 560 570 AACTACACGCTGTGGAACGGGGTGAAAGAAGCACGGCTCCGACTACTCCAAGGAT :::::::::::::::::::::::::::::::::	520 530 540 550 560 570 CACGCTGTCGGAACGGGGTGAAAGAGAAGCACGGCTCCGACTACTCCAAGGAT ::::::::::::::::::::::::::::::::	540 GAAAGAGAAG :::::::::	550 CACGGCTCCG ::::::: CACGGCTCCG 880	560 ACTACTCCAAG ::::::::::: ACTACTCCAAG 890	570 GAT ::: GAT
22437	580 610 620 630 TACCTCACAGACCTCATCACCAATGACAGCGTGAGCTTCTTCCGCACGTCCAAGAAGATG ::::::::::::::::::::::::::::::	580 610 600 610 CACAGACCTCATCACCAATGACAGCGTGAGCTTCT' :::::::::::::::::::::::::::::::::	600 CAGCGTGAGC ::::::::: \CAGCGTGAGC	610 TTCTTCCGCA ::::::::: TTCTTCCGCA	620 CACGTCCAAGAAGAT:::::::::::::::::::::::::	630 ATG ::: ATG

Fig. 31

	640 650 660 670 680 690	
22437	CGC.	- .
1247	. D	r. 0
22437	700 710 720 730 740 750 750 730 740 750 TCAGCCCCACATATTCAGGCCTCTTCCCAAACGCATCTCAGCACTTCACGCCGAGCTAC	\circ
1247	TCAGCCCCACAATATTCACGCCTCTTCCCAAACGCATCTCAGCACATCACGCCGAGCTAC 1080	U O
	0.00 1	0
22437	AACTACGCGCCCAACCCGGACAACACTGGATCATGCGTACACGGGGCCCATGAAGCCC	7)
17.0	: : : : : : : : : : : : : : : : : : :	()
/47	1090 110 1110 1120 1130 114	0
	820 830 840 850 860 870	0 7
22437	ATCCACATGGAATTCACCAACATGCTCCAGCGGAAGCGCTTGCAGACCCTCATGTCGTG	b •
		اح .
1247	ATCCACATGGAATTCACCAACATGCTCCAGCGGAAGCGCTTGCAGACCTCATGTGGTG 1150 1150 1160 1170 1180 1190) 0
	1	

	880	890	006	910	920	930
22437	GACGACTCCATGGAGACGATTTACAACATGCTGGTTGAGACGGGCGAGCTGGACAACACG	SACGATTTACA	ACATGCTGGT1	rgagacgggg	AGCTGGACAAC	ACG
12.47				GAGACGGGCG	GTTGAGACGGGCGAGCTGGACAACAC	::: ACG
/ + 77	1210	1220	1230	1240	1250 1	1260
70700	040	026	960 GTTACCACATI	970 GGCCAGTTTC	940 950 960 970 980 990	990
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1247	TACATCGTATACACO	1280	1290	1300	1310	1320
	1000	1010	1020	1030	1040 1	1050
22437	AAATCCATGCCATA	TGAGTTTGACA	TCAGGGTCCC	GTTCTACGTGA	CCATGCCATATGAGTTTGACATCAGGGTCCCGTTCTACGTGAGGGGCCCCCAACGTG	GTG
					· · · · · · · · · · · · · · · · · · ·	(
1247	AAATCCATGCCATA 1330	TGAGTTTGACA 1340	TCAGGGTCCC 1350	GTTCTACGTGA 1360	CCATGCCATATGAGTTTGACATCAGGGTCCCGTTCTACGTGAGGGGCCCCCAACGTG 1330 1340 1350 1360 1360	1380 1380
	1060	1070	1080	1090	1100 1	.110
22437	GAAGCCGGCTGTCT	GAATCCCCACA	TCGTCCTCAA	CATTGACCTG	CCGGCTGTCTGAATCCCCACATCGTCCTCAACATTGACCTGGCCCCCCACCATCCTG	CTG
			••			•• (
1247	GAAGCCGGCTGTCTGAATCCCCACATCGTCCTCAACATTGACCTGGCCCCCCCATCATG 1200 1200 1400 1410 1420	GAATCCCCACA	TCGTCCTCAA	CATTGACCTG(1420	JCCCCCACCAIC	1440
	1390	つ さ ナ	> + r +)] -{		

Fig. 31

Title: "22437, A Novel Human Sulfatase and Uses Therefor" Inventors: Maria A. Glucksmann et al. U.S. Patent Appl No.: Not Yet Assigned Express Mail # EL665882062US Attorney Docket No. 10147-61U1 Cust # 570

22437	1120 1130 1140 1150 1160 1170 GACATTGCAGGCCTGGACATACCTGCGGATATGGACGGGAAATCCATCC	1130 ACATACCTGC ::::::::::::::::::::::::::::::::::	1140 GGATATGGAC :::::::::::::::::::::::::::::::::::	1150 GGGAAATCC?:::: GGGAAATCC?	1160 ATCCTCAAGCT:::::: ATCCTCAAGCT	1170 CTGCTG ::::: CTGCTG 1500
22437	1180 1190 1200 1210 1220 1230 GACACGGAGCGGCCGGTGAATCGGTTTCACTTGAAAAAGAAGATGAGGGTCTGGCGGGAC :::::::::::::::::::::::::::::::	1190 TGAATCGGTT :::::::::: TGAATCGGTT 1520	1200 TCACTTGAAA :::::::::::::::::::::::::::::::::	1210 AAAGAAGATGA :::::::: AAAGAAGATGA 1540	1220 AGGGTCTGGCG :::::::::	1230 GGAC :::: GGAC 1560
22437	1240 1250 1260 1270 1280 1290 TCCTTCTTGGTGGAGAGGCAAGCTGCTACACAAGAGACAATGACAAGGTGGACGCC ::::::::::::::::::::::::::::::::	1250 GAGGCAAGCT ::::::::: GAGGCAAGCT 1580	1260 GCTACACAA(:::::::: GCTACACAA(1590	1270 SAGAGACAAT(:::::::::: SAGAGACAAT(1600	1280 GACAAGGTGGA ::::::::: GACAAGGTGGA	1290 .c.c.c. .::: .c.c.c.c.
22437	1300 1340 1350 1350 1340 1350 CAGGAGGACCTGTCAGCGTGTGAGGACCTGTGTCAGCGTGTGAGGACCTGTGTCAGCGTGTGAGGACCTGTGTCAGCGTGTGAGGACCTGTGTCAGCGTGTGAGGACCTGTGTCAGCGTGTGAGGACCTGTGTCAGCGTGTGAGGACCTGTGTCAGCGTGTGAGGACCTGTGTCAGCGTGTGAGGACCTGTGTCAGCGTGTGAGGACCTGTGTCAGCGTGTGAGGACCTGTGTCAGCGTGTGAGGACCTGTGTCAGCGTGCTGAGGACCTGTGTCAGCGTGCTGAGGACCTGTGTCAGCGTGCTGAGAGGACCTGTGTCAGCGTGCTGAGAGGACCTGTGTCAGCGTGCTGAGAGGACCTGTGTCAGCGTGCTGAGAGGACCTGTGTCAGCGTGCTGAGAGGACCTGTGTCAGCGTGCTGAGAGAGA	1310 TGCCCAAGTA :::::::: TGCCCAAGTA	1320 CCAGCGTGT ::::::::	1330 SAAGGACCTG ::::::: GAAGGACCTG 1660	1340 TGTCAGCGTGC :::::::::: TGTCAGCGTGC	1350 TGAG:::: TGAG

Fig. 3G

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1.67	\$5.
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miller stands stands among	\$25 \$25 \$25 \$25

	1360	1370	1380	1390	1400	1410
22437	TACCAGACGGCGT::::::TACCAGACGGCGT	cggcgtgtgtgagcagctgggacagaagtggcagtgtgtgt	GGACAGAAGTG ::::::::: GGACAGAAGTG 1710	GCAGTGTGTG ::::::::: GCAGTGTGTG 1720	GAGGACGCCAC ::::::::: GAGGACGCCAC 1730	.:::: ::::::::::::::::::::::::::::::::
22437	1420 1430 1440 1450 1460 1470 AAGCTGAAGCTGCATAAGTGCACCCCTCTCCC :::::::::::::::::::::::::::	420 1430 1440 1450 1460 1470 AGCTGCATAAGTGCAGCCCCCATGCGGCTGGGCGCAGCAGCCCTCTCC ::::::::::::::::::::::::::::::	1440 GGCCCATGCG ::::::::: GGCCCCATGCG	1450 GCTGGGCGGC ::::::::::	1460 AGCAGAGCCCT:::::::::::::::::::::::::::::	1470 FCTCC ::::: FCTCC 1800
22437	1480 1490 1500 1510 1520 1530 AACCTCGTGCCCAAGTACTACGGGCAGGGCAGGGCCTGCACCTGTGACAGCGGGAC ::::::::::::::::::::::::::::	480 1490 1500 1510 1520 1530 TGCCCAAGTACTACGGCCAGGGCAGGCCTGCACCTGTGACAGCGGGGAC :::::::::::::::::::::::::::	1500 CAGGGCAGCG? :::::::::::::::::::::::::::::::::::	1510 .GGCCTGCACC ::::::::	1520 TGTGACAGCGC:::::::::::::::::::::::::::::	1530 3GGAC ::::: 3GGAC
22437	1540 1560 1570 1580 1590 TACAAGCTCAGCCGGACGCCGGAAAAACTCTTCAAGAAGAAGTACAAGGCCAGC ::::::::::::::::::::::::::::	1540 1580 1560 1570 1580 1590 1590 1590 1590 1590 1590 1590 159	1560 CGGAAAAACT ::::::::::::::::::::::::::::::::	1570 rcttcaagaac ::::::::::::::::::::::::::::::::	1580 saagtacaagg :::::::::::::::::::::::::::::::::	1590 CCAGC ::::: CCAGC 1920

Fig. 3F

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	1600	1610	1620	1630	1640	1650
,437	TATGTCCGCAGTCG	CICCAICCGC	TCAGTGGCCAL	CGAGGTGGA	CCGCAGTCGCTCCATCCGCTCAGTGGCCATCGAGGTGGACGGCAGGGTGTACCAC	ACCAC
		••	•••	•••		••
747	TATGTCCGCAGTCG	CTCCATCCGC	TCAGTGGCCA	CGAGGTGGA	CCGCAGTCGCTCCATCCGCTCAGTGGCCCATCGAGGTGGACGGCAGGGTGTACCAC	ACCAC
	1930	1940	1950	1960	1970	1980
	7	7	0	7	7	7.7
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,437	GTAGGCCTGGGTGATGCCGCCCAGCCCCGAAACCTCACCAAGCGGCACTGGCCAGGGGCC	TGCCGCCCAG	CCCGAAACC	rcaccaage	GCACTGGCCAC	30000
	•••	•••		••		••
747	GTAGGCCTGGGGTGATGCCGCCCAGCCCCGAAACCTCACCAAGCGGCACTGGCCAGGGGCC	TGCCGCCCAG	CCCGBAACC	CACCAAGCG	GCACTGGCCAC	229999
	1990	2000	2010	2020	2030	2040
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	1720	1730	1/40	1/20	7 / PO	0//T
1437	CCTGAGGACCAAGATGACAAGGATGGTGGGGACTTCAGTGGCACTGGAGGCCTTCCCGAC	TGACAAGGAT	GGTGGGGACT	CAGTGGCAC	TGGAGGCCTT	CCGAC
		•••	•••			••
247	CCTGAGGACCAAGATGACAAGGATGGTGGGGACTTCAGTGGCACTGGAGGCCTTCCCGAC	TGACAAGGAT	GGTGGGGACT	CAGTGGCAC	TGGAGGCCTT	CCGAC
	2050	2060	2070	2080	2090	2100

Fig. 3]

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22437	1780 TACTCAGCCGCCA :::::::::: TACTCAGCCGCCA	1780 1790 1800 1810 1820 1830 1830 (CCCCCATTAAAGTGACACATCGGTGCTACATCCTAGAGAACGACACACAC	1800 STGACACATCG ::::::::::::::::::::::::::::::::::::	1810 GTGCTACATC(::::::::::::::::::::::::::::::::	1820 CTAGAGAACGA ::::::::::: CTAGAGAACGA 2150	1830 CACA :::: CACA 2160
22437	1840 1850 1860 1870 1880 1890 GTCCAGTGTACAAGTCCCTGCAGGCCTGGAAAGACCACAAGCTGCACACAGCTGCACAGCTGCACAGCTGCACAGCTGCACAGCTGCAGCTGCAGCTGCAGTGTACAAGTCCCTGCAGGCCTGGAAAGACCACAAGCTGCACACAGCTGCAGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCAGCTGCAGCAGCTGCAGCAGCTGCAGCAGCTGCAGCAGCTGCAGCTGCAGCTGCAGCAGCTGCAGCAGCTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	1840 1850 1860 1870 1880 1890 1890 3	1860 AAGTCCCTGCA :::::::::	1870 GGCCTGGAAA(:::::::: GGCCTGGAAA(2200	1880 SACCACAAGCT:::::: SACCACAAGCT	1890 GCAC :::: GCAC 2220
22437	1900 1910 1920 1930 1940 1950 ATCGACCACGAGATTGAAACCCTGCAGAACTTAAGAACCTGAGGGAAGTCCGAGGT ::::::::::::::::::::::::::::::::::	1900 1910 1920 1930 1940 1950 1950 1940 1950 CACGAGATTGAAACCTGCGAGGTTCCGAGGTTCCGAGGTTCCGAGGTTCCGAGGTTCGAGGATTGAGAACCTGAGGGAAGTCCGAGGTTCACGAGATTGAGAACCTGAGGGAAGTCCGAGGTTCAGAGATTAAGAACCTGAGGGAAGTCCGAGGTTCAGAGACCTGAGGGAAGTCCGAGGTTCAGAGTCCGAGGTTCAGAGTCCGAGGTAGATTAAGAACCTGAGGGAAGTCCGAGGTTCAGAGTCCGAGGTTCAGAGTCCGAGGTTCAGAGTCCGAGGTTCAGAGTCCGAGGTTAGAAATTAAGAACCTGAGGGAAGTCCGAGGTTAGAAATTAAGAACCTGAGGGAAGTCCGAGGTAGAGTCCGAGGTAGAGTCCGAGGTAGAGTCCGAGGTAGAAATTAAGAACCTGAGGAAGTCCGAGGTAGAAATTAAGAACCTGAGGAAGTCCGAGGTAGAAAATTAAGAACCTGAGGAAGTCCGAGGTAGAAAATTAAGAACCTGAGGAAGTCCGAGGTAGAAAATTAAGAACCTGAGGAAGTCCGAGGTAGAAAATTAAGAACCTGAGGAAGTCCGAGGTAGAAAATTAAGAACCTGAGGAAGTCCGAGGTAGAAAATTAAGAAACCTGAGGAAGTCCGAGGTAGAAAATTAAGAAACCTGAGGAAGTCCAAGAAAAAAAA	1920 CAGAACAAAT ::::::::::	1930 TAAGAACCTG; ::::::: TAAGAACCTG; 2260	1940 AGGGAAGTCCG :::::::: AGGGAAGTCCG 2270	1950 AGGT :::: AGGT 2280
22437	1960 1970 1980 2000 2010 CACCTGAAGAAAAGCGGCCAGAAGAATGTGACTGTCACAAAATCAGCTACCACACCCAG ::::::::::::::::::::::::::::	1970 AGCGGCCAGAAG :::::::::: AGCGGCCAGAAG 2300	1980 SAATGTGACTG ::::::::: SAATGTGACTG	1990 TCACAAAATC; :::::::: TCACAAAATC; 2320	2000 AGCTACCACAC ::::::::: AGCTACCACAC 2330	2010 CCAG :::: CCAG 2340

Fig. 3.

A CONTRACTOR OF THE CONTRACTOR

	2020	2030	2040	2050	2060	2070
22437	CACAAAGGCCGCCTCAAGCACAGAGGCTCCAGTCTGCATCCTTTCAGGAAGGGCCTGCAA	TCAAGCACAG	AGGCICCAGIC	TGCATCCTTI	CAGGAAGGGCC	TGCAA
1247	::::::::::::::::::::::::::::::::::::::		AGGCTCCAGTCT	TGCATCCTTI	GCATCCTTTCAGGAAGGGCC	GCCTGCAA
1	2350	2360	2370	2380	2390	2400
72/27	2080 2120 2130 2110 2120 2130 2130 2130	2090	2100 3CGGGAGCAGP	2110 AGCGCAAGA	2120 AGAAACTCCGCF	2130 AGCTG
CF477	STATE STATE OF THE PROPERTY OF			AGCGCAAGAZ	CONSTRUCTOR OF THE CONTRACTOR	.:::: AGCTG
/ + 71	2410	2420	2430	2440	2450	2460
	2140	2150	2160	2170	2180	2190
22437	CTCAAGCGCCTGCAGAACAACGACACGTGCAGCCATGCCAGGCCTCACGTGCTTCACCCAC	CAGAACAACGA	CACGTGCAGCA	ATGCCAGGCC	$\mathtt{rcacgrgcttc}$	ACCCAC
	•••	•••	••	••••••		• • • • • • • • • • • • • • • • • • • •
1247	CICAAGCGCCIGCAGAACAACGACACGIGCAGCAIGCCAGGCCICACGIGCIICACCCAC	CAGAACAACGA	CACGIGCAGC	ATGCCAGGCC.	ICACGTGCTTC?	ACCCAC
;	2470	2480	2490	2500	2510	2520
	2200	2210	2220	2230	2240	2250
22437	GACAACCAGCACTGGCAGACGGCGCCTTTCTGGACACTGGGGGCCTTTCTGTGCCTGCACC	TGGCAGACGGC	GCCTTTCTGG2	ACACTGGGGC	CTTTCTGTGCC	rgcacc
	••	••	•••			•••
1247	GACAACCAGCACTGGCAGACGGCGCCTTTCTGGACACTGGGGGCCTTTCTGTGCCTGCC	TGGCAGACGGC	GCCTTTCTGG	ACACTGGGGC	CTTTCTGTGCC	rgcacc
	2530	2540	2550	2560	2570	2580

Fig. 3k

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	2260	2270	2280	2290	2300	2310
22437	AGCGCCAACAATAA	AACAATAACACGTACTGGTGCATGAGGACCATCAATGAGACTCACAATTTCCTC	rgcatgaggac	CATCAATGAG	ACTCACAATTT	CCIC
1247	AGCGCCAACAATAACACGTACTGGTGCATGAGGACCATCAATGAGACTCACTC	**************************************	::::::::::::::::::::::::::::::::::::::	CATCAATGAG	ACTCACAATTT	CCTC
	2590	2600	2610	2620	2630	2640
	2320	2330	2340	2350	2360	2370
22437	TTCTGTGAATTTG	GAATTTGCAACTGGCTTCCTAGAGTACTTTGATCTCAACACAGACCCCTACCAG	CTAGAGTACTI	TGATCTCAAC	ACAGACCCCTA	CCAG
77.7	**************************************					
1471	2650	2660	2670	2680	2690	2700
	2380	2390	2400	2410	2420	2430
22437	CTGATGAATGCAG	JAATGCAGTGAACACACTGGACAGGGATGTCCTCAACCAGCTACACGTACAGCTC	SACAGGGATGI	CCTCAACCAG	CTACACGTACA	CTC
			•••••••••••••••••••••••••••••••••••••••	•••••••••••••••••••••••••••••••••••••••		••
1247	CTGATGAATGCAG	AATGCAGTGAACACACTGGACAGGGATGTCCTCAACCAGCTACACGTACAGCTC	SACAGGGATGI	CCTCAACCAG	CTACACGTACA	CCIC
	2710	2720	2730	2740	2750	2760
	2440	2450	2460	2470	2480	2490
22437	ATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAACCCCCCGGACTCGAAACATGGAC	GCTGCAAGGGT	TACAAGCAGTG	TAACCCCCGG	ACTCGAAACAT	'GGAC
	•••		•••		•••	••
1247	ATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAACCCCCGGACTCGAAACATGGAC	GCTGCAAGGGT	TACAAGCAGTG	TAACCCCCGG	ACTCGAAACAT	GGAC
	2770	2780	2790	2800	2810	2820

Fig. 31

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Express

Title: "22437, A Novel Human Sulfatase and Uses Therefor" Inventors: Maria A. Glucksmann et al. U.S. Patent Appl. No.: Not Yet Assigned

U.S. Patent Appl. No.: Not Yet Assigned Express Mail # EL665882062US Attorney Docket No. 10147-61U1 Cust # 570

20/30

	2500	2510	2520	2530	2540	2550
22437	SACTTAA	AGATGGAGGAAGCTATGAGCAATACAGGCAGTTTCAGCGTCGAAAG'	TGAGCAATAC	AGGCAGTTTC	AGCGTCGAAA	GTGG
1247	CTGGGACTTAAAGA'	GACTTAAAGATGGAGGAAGCTATGAGCAATACAGGCAGTTTCAGCGTCGAAAGTGG	TGAGCAATAC 2850	AGGCAGTITC 2860	AGCGTCGAAA 2870	GTGG 2880
22437	2560 2570 2580 2590 2600 2610 CCAGAAATGAAGACCTTCTTCCAAATCACTGGGACAACTGTGGGAAGGCTGGGAAGGT	2570 ACCTICTICCAA	2580 ATCACTGGG	2590 ACAACTGTGG	2600 aaagctggga	2610 AGGT
1247	CCAGAAATGAAGAG	AAATGAAGAGACCTTCTTCCAAATCACTGGGACAACTGTGGGAAGGCTGGGAAGGT	::::::::	ACAACTGTGGG	:::::::::	AGGT
	2890	2900	2910	2920	2930	2940
22437	TAA				1	
1247	::: TAAGAAACAACAGA	AAACAACAGAGGTGGACCTCCAAAAAATATAGAGGCATCACCTGACTGCACAGGCAA	AAAACATAGA	AGGCATCACCI	GACTGCACAG	GCAA
	7820	0007	0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	N N O	0000

Fig. 3M

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1247	GCAAGCACGCACTCTCAGTCAACATGACAGATTCTGGAGGATAACCAGCAGGAGCAGAGA 3070 3080 3090 3100 3110	ICTCAGTCAACA 3080	TGACAGATTC 3090	TGGAGGATAAC 3100	ccagcaggagc 3110	:AGAGA 3120
22437		! ! ! ! ! !				
1247	TAACTTCAGGAAG 3130	CAGGAAGTCCATTTTGCCTTTTGCTTTGGATTATACCTCACCAGCTGC 3130 3140 3150 3160 3170 3180	CCCTGCTTTT 3150	GCTTTGGATT7 3160	ATACCTCACCA 3170	3180
22437			 	 	 - - - - - - - -	
1247	ACAAAATGCATTTTTCGTATCAAAAGTCACCACATAACCCTCCCCCAGAAGCTCACAAA 3190 3200 3210 3220 3230 3240	ITTTCGTATCAA 3200	AAAGTCACCA 3210	CTAACCCTCCC 3220	CCCAGAAGCTC 3230	acaaa 3240
22437					 	
1247	GGAAAACGGAGAGAGCGAGAGAGATTTCCTTGGAAATTTCTCCCAAGGGCGAAAGT 3300	GAGCGAGCGAGA 3260	GAGATTTCCT 3270	TGGAAATTTC: 3280	ICCCAAGGGCG 3290	SAAAGT 3300

Fig. 3N

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10 L.W. 1014	5 5 5 5 5 5 5 5 5
10 LEN 25 12 25 15 11 LEN	
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22437		 	 	1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	[] !
1247	CATTGGAATTTTT. 3310	AATTTTTAAATCATAGGGGAAAAGCAGTCCTGTTCTAAATCCTCTTATTCTTTT 3310 3320 3330 3340 3350	;AAAAGCAGTC 3330	CTGTTCTAAA 3340	TCCTCTTATTC 3350	3360 3360
22437				 		
1247	GGTTTGTCACAAA 3370	TCACAAAGAAGGAACTAAGAAGCAGGAAGGCCAACGTGGAGAGGCTGAAAAC 3370 3380 3390 3400 3410	AAGCAGGACA 3390	GAGGCAACGT 3400	GGAGAGGCTGA 3410	3420
22437		 	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	 	 	
1247	AGTGCAGAGACGT 3430	GAGACGTTTGACAATGAGTCAGTAGCACAAAAGAGATGACATTTACCTAGCACT 3430 3440 3450 3460 3470 3480	CAGTAGCACA. 3450	AAAGAGATGA 3460	CATTTACCTAC 3470	3480
22437				 		
1247	ATAAACCCTGGTT 3490	CCTGGTTGCCTCTGAAAACTGCCTTCATTGTATATATGTGACTATTTACATG 3490 3500 3510 3520 3530 3540	ACTGCCTTCA' 3510	TTGTATATAT 3520	GTGACTATTTA 3530	ACATG 3540

Fig. 30

22437						ŀ
1247	TAATCAACATGGGA 3550	ACTTTTAGGGGA 3560	AACCTAATAAG 3570	AAATCCCAAT 3580	CAACATGGGAACTTTTAGGGGAACCTAATAAGAAATCCCAATTTTCAGGAGTGGTG 3550 3560 3570 3580 3590 3600	I.G
22437			 	 		!
1247	GTGTCAATAAACGCTCTGTGGCCAGTGTAAAAGAAAATCCCTCGCAGTTGTGGACATTTC 3610 3620 3630 3640 3650 3660	TCTGTGGCCAGI 3620	GTAAAAGAAA 3630	ATCCCTCGC? 3640	AGTTGTGGACATTTC 3650 3660	C 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
22437			! ! ! ! !	 		!
1247	TGTTCCTGTCCAGA 3670	TACCATTTCTCC 3680	TAGTATTTCT 3690	TTGTTATGTC 3700	CCTGTCCAGATACCATTTCTCCTAGTATTTCTTTGTTATGTCCCAGAACTGATGTT 3670 3680 3690 3700 3710 3720	rr 20
22437				 		ļ
1247	TTTTTTTAAGGTA 3730	CTGAAAAGAAAT 3740	GAAGTTGATG 3750	TATGTCCCAP 3760	TTTTAAGGTACTGAAAAGAAATGAAGTTGATGTATGTCCCAAGTTTTGATGAAACT 3730 3740 3750 3760 3770 3780	0 H

Fig. 31

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22437						
1247	GTATTTGTAAAAA 3790	GTAAAAAAATTTTGTAGTTTTAAGTATTGTCATACAGTGTTCAAAACCCCAGCC 3790 3830 3840	TTAAGTATTGT 3810	CATACAGTGT 3820	TCAAAACCCC 3830	AGCC 3840
22437				 		
1247	AATGACCAGCAGT 3850	AATGACCAGCAGTTGGTATGAAGAACCTTTGACATTTTGTAAAAGGCCATTTCTTTC	CCTTTGACATT 3870	TTGTAAAAGG 3880	CCATTTCTTT 3890	CTTG 3900
22437			 	 	 	
1247	GGAGTTTTTTGGT 3910	TTTTGGTGTGTCTGTTTTTTAAAGTATTCAAGATACTACCAGTCAACATCTTT 3910 3920 3930 3940 3950 3960	TTAAAGTATTC 3930	AAGATACTAC 3940	CAGTCAACAT 3950	CTTT 3960
22437						
1247	TIGGAAGAAAAIGCCTIGGGTTIAGAAGAITTTCTTAAAAGGGGAGTAGAIGGTTGTAGA 3970 3980 4000 4000	SCCTTGGGTTTAG 3980	AAGATTTTCTT 3990	AAAAGGGGAG 4000	TAGATGGTTG 4010	TAGA 4020

Fig. 30

,437	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1					[
747	TTGACTAAAAAGTCTACCATACTTCAAGGGACTACAGGTAAGTCTCATAGTATACCAGCT 4030 4040 4050 4060 4070 4080	CTACCATACTTC 4040	CAAGGGACTAC 4050	AGGTAAGTCT(4060	CATAGTATACCAG 4070 40	AGCT 4080
2437			 	 		! !
747	TTGGTACTTCATTTTTAAAAAGTATTAATCAATTGCAAAGAAATTCGCCTTGGCCAAC 4090 4100 4110 4120 4130 4140	TTTTAAAAAGI 4100	rattaatcaat 4110	TGCAAAGAAA 4120	TTCGCCTTGGCCA 4130 41	CAAC 4140
,437						1
747	CCTTCTTTGTGTATCAGGTAGTCTAACCTGATACAAGTTGGTTG	ICAGGTAGTCTA 4160	AACCTGATACA 4170	AGTAGTTGAC? 4180	AGATTTCAACTAT(4190 42)	ATCA 4200
437						
747	ATCACCAGTCCAACCCATTTCTCATTTAACAGATGACGGAGATAATCCCTAAAAGCACCC 4210 4220 4280 4240 4250 4260	CCCATTTCTCAT 4220	ITTAACAGATG 4230	ACGGAGATAA1 4240	FCCCTAAAAGCACCC 4250 4260	09 09

Fig. 3R

Title: "22437, A Novel Human Sulfatase and Uses Therefor"
Inventors: Maria A. Glucksmann et al.
U.S. Patent Appl. No.: Not Yet Assigned
Express Mail # EL665882062US Attorney Docket No. 10147-61U1 Cust # 570

26/30

1247	ACATTTGTTTCAATGCCCCAAACAGGCCAAGGCTCCCTAGCAACTCCCTAGTGGCGTTTTT 4270 4280 4290 4300 4310	TGCCCCAAACAG 4280	GCCAAGGCTC 4290	CCTAGCAACT 4300	CCCTAGTGGC	3TTTT 4320
22437			;] 		
1247	TTAACTTCTCAGAAACTGTTACCATTATTTGAAATAGGCTTCCTTAACCTCCTTTACCCT 4330 4340 4350 4360 4370 4380	AACTGTTACCAT 4340	TATTTGAAA1 4350	AGGCTTCCTT 4360	AACCTCCTTT/ 4370	4380
22437		!				
1247	TAACCCAACAGGGATTT	ATTT				

Fig. 3S

Title: "22437, A Novel Human Sulfatase and Uses Therefor"
Inventors: Maria A. Glucksmann et al.
U.S. Patent Appl. No.: Not Yet Assigned
Express Mail # EL665882062US Attorney Docket No. 10147-61U1 Cust # 570

			10	20	30	40	
22437		MGPPSLV	'LCLLSATVFS	SLLGGSSAFI	SHHRLKGR	MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPN	
1247	NG GING GOG GOG IGNO IGNOS IN CONTRACT IN TAGES AND INCIDENCE TO TWING GOOD AND THE STATE OF THE	NKKKMGDDG1.	IN TABLE TO THE REPORT TO THE TOTAL TO THE REPORT TO THE TO THE TOTAL TO THE TOTAL TO THE THE TOTAL TO T			Mademada	
Ì		20	30	40	50	CALBANTAFIN (0)	
22437	50 60 70 80 90 100 IILVLTDDQDVELGSMQVMNKTRRIMEQGGTHFINAFVTTPMCCPSRSSILTGKYVHNHN	60 LGSMQVMNKT	70 PRIMEQGGTE	80 IFINAFVTTI	90 PMCCPSRSS1	100 LTGKYVHNHN	
1247	::::::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	:::::::	IFINA FVTT	MCCPSRSS1	::::::::::::::::::::::::::::::::::::::	
	70	80	06	100	110	120	
1	110	120	130	140	150	160	
22437		WQAQHESRTF	AVYLNSTGYR	TAFFGKYLN	IEYNGSYVPE	NCSSPSWQAQHESRTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLK	
1247	::::::::::::::::::::::::::::::::::::::	WQAQHESRTE	::::::::	TAFFGKYLN	EYNGSYVPE	::::::::::::::::::::::::::::::::::::::	
	130	140	150	160	170	180	
	170	180	190	200	210	220	
22437		GVKEKHGSDY	SKDYLTDLIT	NDSVSFFRI	SKKMYPHRE	YTLCRNGVKEKHGSDYSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAP	
1247	.:::::::::::::::::::::::::::::::::::::	YTLCRNGVKEKHGSDYSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISH	SKDYLTDLIT	NDSVSFFRI	SKKMYPHRE	::::::::::::::::::::::::::::::::::::::	
	190	200	210	220	230	240	

Fig. 4A

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	230	240	250	260	270	0	280	
22437	HGPEDSAPQYSRLFPNASQHITPSYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQRKRLQ	/SRLFPNAS	ZHITPSYNY <i>P</i>	\PNPDKHWI!	MRYTGPMK	PIHMEFT	NMLQRKRLQ	
1247	HGPEDSAPQYSRLFPNASQHITPSYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLORKRLO	SRLFPNAS	HITPSYNY?	PNPDKHWII	 MRYTGPMK	PIHMEFT	::::::: NMLORKRLO	
	250) 2(260 2	270	280	290	300	
		300	310	320	330	0	340	
75427	THASUDVAMIT.	T.T. A UMIT A T.T.	SMETTYNMLVETGELDNTYIVYTADHGYHIGQFGLVKGKSMPYEFDIRVPFYV	YTADHGYH	IGQFGLVK	GKSMPYE	FDIRVPFYV	
1247	TLMSVDDSMETIYNMLVETGELDNTYIVYTADHGYHIGQFGLVKGKSMPYEFDIRVPFYV	TIYNMLVE	GELDNTYIV	YTADHGYH.	IGQFGLVK	GKSMPYE	FDIRVPFYV	
	310	32	320 3	330	340	350	360	
	350	360	370	380	390	0	400	
22437	RGPNVEAGCLNPHIVLNIDLAPTILDIAGLDIPADMDGKSILKLLDTERPVNRFHLKKKM	NPHIVLNI	CAPTILDIA	GLDIPADMI	OGKSILKL	LDTERPVI	NRFHLKKKM	
1247	RGPNVRAGCINDHIVINIDIAPTIIDIACIDIDADMOCKSTIKIIOTEDINDEUT KEW	T L N T L T H d N.	COLINDHIVINITIA PUTITIA DI BADMACKSTI KIT KIT KIT BENINDENI KAKAMA	INT Z T T T T				
:	370	38	380	390	400	410	420	
	410	420	030	0 7 7	\ \ \	ے	0	
22437	건	IES RGKLLHKRI	TVERGKLLHKRDNDKVDAQEENFLPKYQRVKDLCQRAEYQTACEQLGQKWQCV	440 NFLPKYQRI	49 /KDLCQRAI	S EYQTACE(400 QLGQKWQCV	
	•••	•••	••	••	•••	••	••	
1247	RVWRDSFLVERGKLLHKRDNDKVDAQEENFLPKYQRVKDLCQRAEYQTACEQLGQKWQCV	RGKLLHKRL	NDKVDAQEE	NFLPKYQR\	/KDLCQRA	EYQTACE	OLGQKWQCV	
	430	440	10 4	450	460	470	480	

Fig. 4B

	470	480	490	500	510	520	
22437	EDATGKLKLH	KCKGPMRLG	KLHKCKGPMRLGGSRALSNLVPKYYGQGSEACTCDSGDYKLSLAGRRKKLFKK	YYGQGSEA(CTCDSGDYF	KLSLAGRRKKI	FKK
1247	::::::: EDATGKLKLH	:::::: KCKGPMRLG	*:::::::::::::::::::::::::::::::::::::	YYGQGSEAC	TCDSGDYF	::::::::::::::::::::::::::::::::::::::	 FKK
	490	200	0 510	52	520	530	540
22437	530 KYKASYVRSR	540 SIRSVAIEV	540 580 570 580 RSRSIRSVAIEVDGRVYHVGLGDAAQPRNLTKRHWPGAPEDQDDKDGGDFSGT	560 AAQPRNLTE	570 KRHWPGAPE	580 DQDDKDGGDI	ISGT
1247	KYKASYVRSR	SIRSVAIEV	:::::: GRVYHVG	AAQPRNLTE	KRHWPGAPE	::::::::::::::::::::::::::::::::::::::	::: 18GT
	550	560	610	009	580	590	009
22437	S	SSS PIKVTHRCY	AANPIKVTHRCYILENDTVQCDLDLYKSLQAWKDHKLHIDHEIETLQNKIKNL	UZS DLYKSLQAW	OSO IKDHKLHID	640 HEIETLQNK1	KNL
1247	::::::::::::::::::::::::::::::::::::::	::::::: PIKVTHRCY	::::::::::::::::::::::::::::::::::::::	::::::DLYKSLQAW	::::::: /KDHKLHID	HEIETLONKI	::: KNL
	610	620	0 630	640	0.1	650	099
	650	099	029	089	069	700	
22437	REVRGHLKKK	RPEECDCHK •••••••	KKKRPEECDCHKISYHTQHKGRLKHRGSSLHPFRKGLQEKDKVWLLREQKRKK	KHRGSSLHF •••••••	FRKGLQEK	DKVWLLREQE	RKK
1247	REVRGHLKKK	RPEECDCHK	REVRGHLKKKRPEECDCHKISYHTQHKGRLKHRGSSLHPFRKGLQEKDKVWLLREQKRKK	KHRGSSLHF	······· FRKGLQEK	DKVWLLREQE	··· RKK
	029	089	069 0	700	0.0	710	720

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Fig. 4(

22437	710 KLRKLLKRLQN :::::::: KLRKLLKRLQN 730	720 DNNDTCSM :::::::	73(PGLTCFTI PGLTCFTI 740	0 HDNQHWQ1 HDNQHWQ1 750	740 :APEWTLGP: ::::::::	750 FCACTSANI ::::::: FCACTSANI	710 720 730 740 750 760 KLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLGPFCACTSANNNTYWCMRTINE ::::::::::::::::::::::::::::::::::::
22437 1247	770 THNFLFCEFA' ::::::: THNFLFCEFA' 790	780 ATGFLEYF :::::::	790 1914 1917 1908 1914 1917 1918 1919) 2LMNAVNT :::::::: 2LMNAVNT 810	800 'LDRDVLNQI ::::::::::::::::::::::::::::::::::::	810 LHVQLMEL] ::::::: LHVQLMEL]	770 780 800 810 820 THNFLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQLHVQLMELRSCKGYKQCNPR ::::::::::::::::::::::::::::::::::::
22437	830 840 850 860 870 TRNMDLGLKDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG :::::::::::::::::::::::::::::::::	840)GGSYEQY: ::::::::	850 RQFQRRKWI:::::: RQFQRRKWI) WPEMKRPS ::::::: WPEMKRPS 870	0 840 850 860 870 DLGLKDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG :::::::::::::::::::::::::::::::::	870 :::::	

Fig. 4D

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